

SEQUENCE LISTING

- (1) GENERAL INFORMATION
 - (i) APPLICANT: Goli, Surya K.
Hillman, Jennifer L.
Murry, Lynn E.
 - (ii) TITLE OF THE INVENTION: NOVEL HUMAN CYTOKINE/STEROID
RECEPTOR PROTEIN
 - (iii) NUMBER OF SEQUENCES: 4
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 94304
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0233 US
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
 - (C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 220 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: CONUTUT01

(B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
 1           5           10           15
Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
 20           25           30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
 35           40           45
Asp Gln Pro Ala Ala Ser Gly Asp Arg Thr Thr Thr Xaa Pro Pro Pro
 50           55           60
Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
 65           70           75           80
Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
 85           90           95
Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
 100          105          110
Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
 115          120          125
Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
 130          135          140
Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe
 145          150          155          160
Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu
 165          170          175
Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ser Arg
 180          185          190
Lys Asn Val Lys Ala Phe Ser Gly Ser Ile Ser Xaa Xaa Tyr Phe Ala
 195          200          205
Lys Ser Phe Val Thr Val His Xaa Val Phe Lys Thr
 210          215          220

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: CONUTUT01
- (B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GCCGCCGAAC CCCGCGCGCC ACTCGCTCGC TCAGAGGGAG GAGAAAGTGG CGAGTTCGG 60
ATCCCTGCCT AGCGCGGCCC AACCTTTACT CCAGAGATCA TGGCTGCCGA GGATGTGGTG 120
GCGACTGGCG CCGACCCAAG CGATCTGGAG AGCGGCGGGC TGCTGCATGA GATTTTCACG 180
TCGCCGCTCA ACCTGCTGCT GCTTGGCCTC TGCATCTTCC TGCTCTACAA GATCGTGCGC 240
GGGGACCAGC CGGCGGCCAG CGGCGACAGG ACGACGACGA NGCCGCCCCC TCTGCCCCGC 300
CTCAAGCGGC GCGACTTCAC CCCCGCCGAG CTGCGGCGCT TCGACGGCGT CCAGGACCCG 360
CGCATACTCA TGGCCATCAA CGGCAAGGTG TTCGATGTGA CCAAAGGCCG CAAATTCTAC 420
GGGCCCCGAGG GGCCGTATGG GGTCTTTGCT GGAAGAGATG CATCCAGGGG CCTTGCCACA 480
TTTTGCCTGG ATAAGGAAGC ACTGAAGGAT GAGTACGATG ACCTTTCTGA CCTCACTGCT 540
GCCCCAGCAGG AGACTCTGAG TGAAGGAGG TCTCAGTTCA CTTTCAAGTA TCATCACGTG 600
GGCAAAGTGC TGAAGGAGGG GGAGGAGCCC ACTGTGTACT CAGATGAGGA AGAACCAAAA 660
GATGAGAGTT CCCGGA AAAA TGTAAAGCA TTCAGTGGA GTATATCTAT NNTGTATTTT 720

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GCAAAATCAT TTGTAACAGT CCACTNTGTC TTAAACAT AGTGTTACAA TATTTAGAAA 780
 GTTTGAGC 788

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1518818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Ala	Glu	Asp	Val	Val	Ala	Thr	Gly	Ala	Asp	Pro	Ser	Glu	Leu	1	5	10	15
Glu	Gly	Gly	Gly	Leu	Leu	Gln	Glu	Ile	Phe	Thr	Ser	Pro	Leu	Asn	Leu	20	25	30	
Leu	Leu	Leu	Gly	Leu	Cys	Ile	Phe	Leu	Leu	Tyr	Lys	Ile	Val	Arg	Gly	35	40	45	
Asp	Gln	Pro	Gly	Ala	Ser	Gly	Asp	Asn	Asp	Asp	Asp	Glu	Pro	Pro	Pro	50	55	60	
Leu	Pro	Arg	Leu	Lys	Pro	Arg	Asp	Phe	Thr	Pro	Ala	Glu	Leu	Arg	Arg	65	70	75	80
Tyr	Asp	Gly	Val	Gln	Asp	Pro	Arg	Ile	Leu	Met	Ala	Ile	Asn	Gly	Lys	85	90	95	
Val	Phe	Asp	Val	Thr	Lys	Gly	Arg	Lys	Phe	Tyr	Gly	Pro	Glu	Gly	Pro	100	105	110	
Tyr	Gly	Val	Phe	Ala	Gly	Arg	Asp	Ala	Ser	Arg	Gly	Leu	Ala	Thr	Phe	115	120	125	
Cys	Leu	Asp	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Tyr	Asp	Asp	Leu	Ser	Asp	130	135	140	
Leu	Thr	Pro	Ala	Gln	Gln	Glu	Thr	Leu	Asn	Asp	Trp	Asp	Ser	Gln	Phe	145	150	155	160
Ser	Ser	Pro	Ser	Ser	Thr	Ile	Thr	Trp	Gly	Lys	Leu	Leu	Glu	Gly	Ala	165	170	175	
Glu	Glu	Pro	Ile	Val	Tyr	Ser	Asp	Asp	Glu	Glu	Gln	Lys	Met	Arg	Leu	180	185	190	
Leu	Gly	Arg	Val	Thr	Glu	Ala	Val	Ser	Gly	Ala	Tyr	Leu	Phe	Leu	Tyr	195	200	205	
Phe	Ala	Lys	Ser	Phe	Val	Thr	Phe	Gln	Ser	Val	Phe	Thr	Thr	Trp		210	215	220	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1657409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

PF-0233-2 CON

Met	Ala	Ala	Glu	Asp	Val	Ala	Ala	Thr	Gly	Ala	Asp	Pro	Ser	Glu	Leu
1				5					10					15	
Glu	Gly	Gly	Gly	Leu	Leu	His	Glu	Ile	Phe	Thr	Ser	Pro	Leu	Asn	Leu
			20					25					30		
Leu	Leu	Leu	Gly	Leu	Cys	Ile	Phe	Leu	Leu	Tyr	Lys	Ile	Val	Arg	Gly
		35					40					45			
Asp	Gln	Pro	Ala	Ala	Ser	Asp	Ser	Asp	Asp	Asp	Glu	Pro	Pro	Pro	Leu
	50					55					60				
Pro	Arg	Leu	Lys	Arg	Arg	Asp	Phe	Thr	Pro	Ala	Glu	Leu	Arg	Arg	Phe
65					70					75					80
Asp	Gly	Val	Gln	Asp	Pro	Arg	Ile	Leu	Met	Ala	Ile	Asn	Gly	Lys	Val
				85				90						95	
Phe	Asp	Val	Thr	Lys	Gly	Arg	Lys	Phe	Tyr	Gly	Pro	Glu	Gly	Pro	Tyr
			100					105						110	
Gly	Val	Phe	Ala	Gly	Arg	Asp	Ala	Ser	Arg	Gly	Leu	Ala	Thr	Phe	Cys
		115					120					125			
Leu	Asp	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Tyr	Asp	Asp	Leu	Ser	Asp	Leu
	130					135					140				
Thr	Pro	Ala	Gln	Gln	Glu	Thr	Leu	Asn	Asp	Trp	Asp	Ser	Gln	Phe	Thr
145					150					155					160
Phe	Lys	Tyr	His	His	Val	Gly	Lys	Leu	Leu	Lys	Glu	Gly	Glu	Glu	Pro
				165				170						175	
Thr	Val	Tyr	Ser	Asp	Glu	Glu	Glu	Pro	Lys	Asp	Glu	Ser	Ala	Arg	Lys
			180					185					190		
Asn	Asp														